

WHAT IS CLAIMED IS:

1. An isolated or recombinant polynucleotide encoding at least a portion of a *Helicobacter* glycosyltransferase involved in the biosynthesis of a *Helicobacter* lipopolysaccharide (LPS).
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2. A polynucleotide according to claim 1, wherein the glycosyltransferase is involved in the biosynthesis of the O-chain region of the LPS.
- 10 3. A polynucleotide according to claim 1, wherein the glycosyltransferase is involved in the biosynthesis of the core region of the LPS.
4. A polynucleotide according to claim 2, wherein the glycosyltransferase is a galactosyltransferase.
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5. A polynucleotide according to claim 4, wherein the galactosyltransferase is a β -1,4-galactosyltransferase.
6. A polynucleotide according to claim 5, wherein the *Helicobacter* is a strain of *H. pylori*.
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7. A polynucleotide according to claim 3, wherein the glycosyltransferase is a glucosyltransferase.
- 25 8. A polynucleotide according to claim 7, wherein the glycosyltransferase is an α -1,6-glucosyltransferase.
9. A polynucleotide according to claim 8, wherein the *Helicobacter* is a strain of *H. pylori*.
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10. A polynucleotide according to claim 3, wherein the glycosyltransferase is a heptosyltransferase.

11. A polynucleotide according to claim 10, wherein the heptosyltransferase is an ADP-heptose-LPS heptosyltransferase II.
12. A polynucleotide according to claim 11, wherein the *Helicobacter* is a strain of *H. pylori*.
13. An isolated or recombinant polynucleotide having sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 and fragments and variants thereof.
14. An isolated or recombinant polynucleotide having at least about 70% identity to the polynucleotide according to claim 13.
15. An isolated or recombinantly produced polypeptide comprising at least a portion of a *Helicobacter* glycosyltransferase involved in the biosynthesis of a *Helicobacter* lipopolysaccharide (LPS).
16. A polypeptide according to claim 15, wherein the glycosyltransferase is involved in the biosynthesis of the O-chain region of the LPS.
17. A polypeptide according to claim 15, wherein the glucosyltransferase is involved in the biosynthesis of the core region of the LPS.
18. A polypeptide according to claim 16, wherein the glycosyltransferase is a galactosyltransferase.
19. A polypeptide according to claim 18, wherein the galactosyltransferase is a β -1,4-galactosyltransferase.
20. A polypeptide according to claim 19, wherein the *Helicobacter* is a strain of *H. pylori*.

21. A polypeptide according to claim 17, wherein the glycosyltransferase is a glucosyltransferase.
22. A polypeptide according to claim 21, wherein the glucosyltransferase is an
5 α -1,6-glucosyltransferase.
23. A polypeptide according to claim 22, wherein the *Helicobacter* is a strain of *H. pylori*.
- 10 24. A polypeptide according to claim 17, wherein the glycosyltransferase is a heptosyltransferase.
25. A polypeptide according to claim 24, wherein the heptosyltransferase is an ADP-heptose-LPS heptosyltransferase II.
- 15 26. A polypeptide according to claim 24, wherein the *Helicobacter* is a strain of *H. pylori*.
27. An isolated or recombinantly produced polypeptide having sequence
20 selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 and fragments and variants thereof.
28. An isolated or recombinantly produced polypeptide having at least about
25 50% identity to the isolated polypeptide according to claim 27.
29. A recombinant vector comprising a nucleic acid encoding at least a portion of a *Helicobacter* glycosyltransferase involved in the biosynthesis of a *Helicobacter* lipopolysaccharide (LPS).
- 30 30. A recombinant vector according to claim 29, wherein the glycosyltransferase is involved in the biosynthesis of the O-chain region of the LPS.

31. A recombinant vector according to claim 29, wherein the glycosyltransferase is involved in the biosynthesis of the core region of the LPS.

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32. A recombinant vector according to claim 30, wherein the glycosyltransferase is a galactosyltransferase.

33. A recombinant vector according to claim 32, wherein the
10 galactosyltransferase is a β -1,4-galactosyltransferase.

34. A recombinant vector according to claim 33, wherein the *Helicobacter* is a strain of *H. pylori*.

15 35. A recombinant vector according to claim 31, wherein the glycosyltransferase is a glucosyltransferase.

36. A recombinant vector according to claim 35, wherein the glucosyltransferase is an α -1,6-glucosyltransferase.

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37. A recombinant vector according to claim 36, wherein the *Helicobacter* is a strain of *H. pylori*.

38. A recombinant vector according to claim 31, wherein the
25 glycosyltransferase is a heptosyltransferase.

39. A recombinant vector according to claim 38, wherein the heptosyltransferase is an ADP-heptose-LPS heptosyltransferase II.

30 40. A recombinant vector according to claim 39, wherein the *Helicobacter* is a strain of *H. pylori*.

41. A recombinant vector according to claim 29, wherein the glycosyltransferase has a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 and fragments and variants thereof.

42. An expression cassette that comprises a nucleic acid encoding at least a portion of a *Helicobacter* glycosyltransferase involved in the biosynthesis of a *Helicobacter* lipopolysaccharide (LPS).

43. An expression cassette according to claim 42, wherein the glycosyltransferase is involved in the biosynthesis of the O-chain region of the LPS.

44. An expression cassette according to claim 42, wherein the glycosyltransferase is involved in the biosynthesis of the core region of the LPS.

45. An expression cassette according to claim 42, wherein the glycosyltransferase has a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 and fragments and variants thereof.

46. A host cell comprising a recombinant nucleic acid which can express a protein encoding at least a portion of a *Helicobacter* glycosyltransferase involved in the biosynthesis of a *Helicobacter* lipopolysaccharide (LPS).

47. A host cell according to claim 46, wherein the glycosyltransferase is involved in the biosynthesis of the O-chain region of the LPS.

48. A host cell according to claim 46, wherein the glycosyltransferase is involved in the biosynthesis of the core region of the LPS.

49. A host cell according to claim 46, wherein the glycosyltransferase has a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 and fragments and variants thereof.

50. A host cell according to claim 49, wherein the cell is a eukaryotic cell.

51. A host cell according to claim 49, wherein the cell is a prokaryotic cell.

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52. A host cell according to claim 51, wherein the prokaryotic cell is a cell of *E. coli*.

53. A method for producing a polypeptide comprising at least a portion of a *Helicobacter* glycosyltransferase involved in the biosynthesis of a *Helicobacter* lipopolysaccharide (LPS), comprising the steps of maintaining a host cell of claim 46 under conditions suitable for expression of said polypeptide and recovering the polypeptide so produced.

54. A method according to claim 53, wherein the glycosyltransferase has a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 and fragments and variants thereof.

55. A method according to claim 53, further including the step of purifying the recovered polypeptide.

56. A hybridization probe comprising a portion of a polynucleotide encoding a *Helicobacter* glycosyltransferase involved in the biosynthesis of a *Helicobacter* lipopolysaccharide (LPS).

57. A hybridization probe according to claim 56, wherein the glycosyltransferase has a sequence selected from the group consisting of

SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 and fragments and variants thereof.

5 58. A hybridization probe according to claim 57, wherein the probe comprises at least about 15 nucleotides.

59. A mutant strain of *H. pylori*, said mutant strain having deactivated at least one gene encoding a glycosyltransferase involved in the biosynthesis of a *H.*
10 *pylori* lipopolysaccharide (LPS).

60. A mutant strain according to claim 59, wherein the glycosyltransferase is involved in the biosynthesis of the O-chain of the LPS.

15 61. A mutant strain according to claim 59, wherein the glycosyltransferase is involved in the biosynthesis of the core region of LPS.

62. A mutant according to claim 59, wherein the glycosyltransferase is coded by open reading frames 0826, 0159, 0479 or 1191.

20 63. A vaccine composition comprising an antigen derived from a mutant strain of *H. pylori* according to claim 59.

64. A vaccine composition according to claim 63, wherein the antigen is an at
25 least partially purified lipopolysaccharide.

65. A vaccine composition according to claim 64, wherein the antigen is conjugated to a protein.

30 66. A live attenuated vaccine composition comprising a mutant strain of *H. pylori* according to claim 59.

67. A reaction mixture for an enzymatic synthesis of a *Helicobacter* lipopolysaccharide or a portion thereof, the mixture comprising an isolated polypeptide having activity of a *Helicobacter* glycosyltransferase involved in the biosynthesis of a *Helicobacter* lipopolysaccharide (LPS).

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68. A reaction mixture according to claim 67, wherein the glycosyltransferase is involved in the biosynthesis of the O-chain region of the *Helicobacter* lipopolysaccharide.

10 69. A reaction mixture according to claim 67, wherein the glycosyltransferase is involved in the biosynthesis of the core region of the *Helicobacter* lipopolysaccharide.

15 70. A reaction mixture according to claim 66, wherein the bacterial lipopolysaccharide is a mimic of a *Helicobacter* lipopolysaccharide.